<110> MEIJI SEIKA KAISHA, LTD.

<120> Endoglucanase and cellulase composition containing the same

<130> 121659PX

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<150> JP302387/1998

<151> 1998-10-23

<160> 113

<170> PatentIn Ver. 2.0

<210> 1

<211> 338

<212> PRT

<213> Rhizopus oryzae CP96001

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<222> (1)...(315)

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Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser
 10                 15                  20                  25

Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Ser Gly
                30                  35                  40

Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys Lys Thr Thr Thr
            45                  50                  55

Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr
        60                  65                  70

Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala Ser Thr Pro Ser
     75                  80                  85

Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala Val Ser Gly Gly
 90                 95                  100                 105

Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala
                110                 115                 120
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Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser
125 130 135

Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser Asn Ala Gln Ser
140 145 150

Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp
155 160 165

Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser
170 175 180 185

Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe
190 195 200

Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val Gln Val Thr Asn
205 210 215

Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln
220 225 230

Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln Trp
235 240 245

Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser
250 255 260 265

Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys

270 275 280

Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr
285 290 295

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300 305 310

Arg Lys
315

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<212> DNA
<213> Rhizopus oryzae CP96001

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Gly Thr Glu Met Ala Ser Ala Ala Glu Cys Ser Lys Leu Tyr Gly Gln

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tgt ggt ggt aag aac tgg aat ggc cct act tgt tgt gaa tct gga tcc 144
Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser
10 15 20 25

acc tgt aaa gta agc aac gat tac tac tct caa tgt ctt ccc tct gga 192
Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Ser Gly
30 35 40

agc agt ggc aat aaa tct tct gaa agt gct cac aag aag act acc act 240
Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys Lys Thr Thr Thr
45 50 55

gct gct cac aag aag act act acc gct gct cat aaa aag act acc act 288
Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr
60 65 70

gct cct gct aag aag act aca act gtt gcc aaa gct tcc acc cct tct 336
Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala Ser Thr Pro Ser
75 80 85

aac tct agc tct agc tcc agc ggc aaa tat tcc gct gtc tct ggt ggt 384
Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala Val Ser Gly Gly
90 95 100 105

gcc tct ggt aac ggt gtc act act cgt tat tgg gat tgc tgt aag gcc 432
Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala
110 115 120

tcc tgt agc tgg ccc ggt aag gcc aat gtc agt tct cct gtc aag tcc 480
Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser
125 130 135

tgt aac aaa gat ggt gtc act gcc ctt agt gac agc aat gcc caa agt 528
Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser Asn Ala Gln Ser
140 145 150

ggc tgt aac ggt ggt aac agt tac atg tgt aac gac aac caa cct tgg 576
Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp
155 160 165

gct gta aac gac aac ctt gcc tat ggt ttc gct gct gct gcc atc agt 624
Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser
170 175 180 185

ggt ggt ggt gaa tct cgc tgg tgc tgt tct tgt ttc gaa ctt act ttc 672
Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe
190 195 200

act tct acc tct gtt gct ggt aag aag atg gtt gtc caa gtc act aac 720
Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val Gln Val Thr Asn
205 210 215

act ggt ggt gat ctt ggc tcc tct act ggt gct cac ttt gac ttg caa 768
Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln
220 225 230

atg ccc ggt ggt ggt gtt ggt att ttc aat ggt tgt tcc agc caa tgg 816
Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln Trp
235 240 245

ggt gct ccc aat gac ggt tgg ggc tca aga tac ggt ggt att tct tct 864
Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser
250 255 260 265

gca tct gac tgc tct agt ctt cct tcc gca ctc caa gct ggt tgt aaa 912
Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys
270 275 280

tgg aga ttc aac tgg ttc aag aac gct gat aac cca agc atg act tac 960
Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr
285 290 295

aag gaa gtt acc tgt cct aag gaa atc acc gcc aag aca ggt tgt tca 1008
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300 305 310

aga aaa taa 1017
Arg Lys
315

<210> 3
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<213> Rhizopus oryzae CP96001

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<222> (-23)...(-1)

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Cys Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser
10 15 20 25

Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu
30 35 40

Ser Asn Gly Asn Lys Ser Ser Glu Cys Ser Lys Leu Tyr Gly Gln Cys
45 50 55

Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr
60 65 70

Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu Ser
75 80 85

Asn Gly Asn Lys Thr Ser Glu Ser Ala His Lys Thr Thr Thr Thr Thr

90 95 100 105

Ala Pro Ala Lys Glu Ile Thr Thr Thr Ala Lys Ala Ser Asn Ser Ser
110 115 120

Asn Ser Ser Gly Lys Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly Asn
125 130 135

Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala Ser Cys Ser Trp
140 145 150

Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser Cys Asn Lys Asp
155 160 165

Gly Val Thr Ala Leu Ser Asp Ser Asn Val Gln Ser Gly Cys Asn Gly
170 175 180 185

Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp Ala Val Asn Asp
190 195 200

Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser Gly Gly Gly Glu
205 210 215

Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe Thr Ser Thr Ser
220 225 230

Val Ala Gly Lys Lys Met Val Ile Gln Val Thr Asn Thr Gly Gly Asp
235 240 245

Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln Met Pro Gly Gly
250 255 260 265

Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Gly Ala Pro Asn
270 275 280

Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys
285 290 295

Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys Trp Arg Phe Asn
300 305 310

Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys Glu Val Thr
315 320 325

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<210> 4

<211> 1101

<212> DNA

<213> Rhizopus oryzae CP96001

<220>

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Gly Thr Glu Met Ala Ser Ala Ala Lys Cys Ser Lys Leu Tyr Gly Gln
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tgt ggt ggt aag gac tgg aat ggc cct act tgt tgc gaa tct gga tcc 144
Cys Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser
10 15 20 25

acc tgt aaa gta agc aac gat tac tac tct caa tgt ctt gcc cct gaa 192
Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu
30 35 40

agc aac ggc aat aag tct tct gaa tgt agc aag ttg tat ggt caa tgt 240
Ser Asn Gly Asn Lys Ser Ser Glu Cys Ser Lys Leu Tyr Gly Gln Cys
45 50 55

ggt ggt aag gac tgg aat ggc cct act tgt tgc gaa tct gga tcc acc 288
Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr
60 65 70

tgt aaa gta agc aac gat tac tac tct caa tgt ctt gcc cct gaa agc 336
Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu Ser
75 80 85

aat ggc aat aaa act tct gaa agc gct cat aaa acg act act acc act 384
Asn Gly Asn Lys Thr Ser Glu Ser Ala His Lys Thr Thr Thr Thr Thr
90 95 100 105

gct ccc gct aag gaa att aca act act gcc aaa gct tca aac tct tct 432
Ala Pro Ala Lys Glu Ile Thr Thr Thr Ala Lys Ala Ser Asn Ser Ser
110 115 120

aac tct agc ggc aaa tac tcc att gtc tct ggt ggt gcc tct ggt aac 480
Asn Ser Ser Gly Lys Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly Asn
125 130 135

ggt gtc act act cgt tat tgg gat tgc tgt aag gcc tcc tgt agc tgg 528
Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala Ser Cys Ser Trp
140 145 150

ccc ggt aag gcc aat gtc agt tct cct gtc aag tcc tgt aac aaa gat 576
Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser Cys Asn Lys Asp
155 160 165

ggt gtc act gcc ctt agt gac agc aat gtc caa agt ggc tgt aac ggt 624
Gly Val Thr Ala Leu Ser Asp Ser Asn Val Gln Ser Gly Cys Asn Gly
170 175 180 185

ggt aac agt tac atg tgt aac gac aac cag cct tgg gct gta aac gat 672
Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp Ala Val Asn Asp
190 195 200

aat ctt gcc tat ggt ttc gct gct gct gcc atc agt ggt ggt ggt gaa 720

Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser Gly Gly Gly Glu
205 210 215

tct cgc tgg tgc tgt tct tgt ttc gaa ctt act ttc act tct acc tct 768
Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe Thr Ser Thr Ser
220 225 230

gtt gct ggt aag aag atg gtt atc caa gtc act aac act ggt ggt gat 816
Val Ala Gly Lys Lys Met Val Ile Gln Val Thr Asn Thr Gly Gly Asp
235 240 245

ctt ggc tcc tct act ggt gct cac ttt gac ttg caa atg ccc ggt ggt 864
Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln Met Pro Gly Gly
250 255 260 265

ggt gtt ggt att ttc aat ggt tgc tcc aag caa tgg ggt gct ccc aat 912
Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Gly Ala Pro Asn
270 275 280

gac ggt tgg ggc tcg aga tac ggt ggt att tct tct gca tct gac tgc 960
Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys
285 290 295

tct agt ctt cct tcc gca ctc caa gct ggt tgt aaa tgg aga ttc aac 1008
Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys Trp Arg Phe Asn
300 305 310

tgg ttc aag aac gct gat aac cca agc atg act tac aag gaa gtt acc 1056
Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys Glu Val Thr

315 320 325

tgt ccc aag gaa atc acc gcc aag aca ggt tgt tca aga aaa taa 1101
Cys Pro Lys Glu Ile Thr Ala Lys Thr Gly Cys Ser Arg Lys
330 335 340

<210> 5
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<213> Rhizopus oryzae CP96001

<220>
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Cys Gly Gly Lys Asn Trp Asp Gly Pro Thr Cys Cys Glu Ser Gly Ser
10 15 20 25

Thr Cys Val Asp Tyr Pro Asp Asn Pro Phe Tyr Ser Gln Cys Val Pro
30 35 40

Asn Glu Asn Leu Thr Ser Thr Asn Lys Ser Ser His Lys Thr Thr Thr
45 50 55

Thr Glu Ser Ala Lys Lys Thr Thr Thr Thr Lys Gly Ser Lys Lys Thr
60 65 70

Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Glu Ala Ser Lys
75 80 85

Lys Thr Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Thr Lys
90 95 100 105

Lys Ala Ser Thr Ser Thr Ser Ser Ser Ser Ser Ser Ala Ser Thr Asn
110 115 120

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly Asn Gly Glu Thr Thr Arg
125 130 135

Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ser Trp Pro Gly Lys Ala Asp
140 145 150

Val Thr Ser Pro Val Gly Ser Cys Asn Lys Asp Gly Lys Thr Leu Ala
155 160 165

Asp Asn Asn Thr Gln Asn Gly Cys Val Gly Gly Ser Ser Tyr Thr Cys
170 175 180 185

Asn Asp Asn Gln Pro Trp Val Val Ser Asp Asp Leu Ala Tyr Gly Phe

190 195 200

Ala Ala Ala Ser Ile Ser Gly Gly Ser Glu Ala Thr Trp Cys Cys Ala
205 210 215

Cys Phe Glu Leu Thr Phe Thr Ser Thr Ala Val Lys Gly Lys Lys Met
220 225 230

Val Val Gln Val Thr Asn Thr Gly Ser Asp Leu Gly Ser Asn Thr Gly
235 240 245

Ala His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Tyr Asn
250 255 260 265

Gly Cys Ala Thr Gln Trp Gly Ala Pro Thr Asp Gly Trp Gly Ala Arg
270 275 280

Tyr Gly Gly Val Ser Ser Ala Ser Asp Cys Ser Asn Leu Pro Ser Ala
285 290 295

Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn Ala Asp
300 305 310

Asn Pro Thr Met Thr Tyr Lys Gln Val Thr Cys Pro Lys Ala Ile Thr
315 320 325

Ala Lys Ser Gly Cys Ser Arg Lys
330 335

<210> 6

<211> 1083

<212> DNA

<213> Rhizopus oryzae CP96001

<220>

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<221> mat_peptide

<222> (70)..(1083)

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-20 -15 -10

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Gly Thr Glu Met Ala His Ala Ala Glu Cys Ser Lys Ala Tyr Tyr Gln
-5 1 5

tgt ggt ggt aag aac tgg gat gga cct acc tgc tgt gaa tct ggc tct 144
Cys Gly Gly Lys Asn Trp Asp Gly Pro Thr Cys Cys Glu Ser Gly Ser
10 15 20 25

act tgc gtt gat tat cct gac aat cct ttc tac tcc caa tgt gtt ccc 192
Thr Cys Val Asp Tyr Pro Asp Asn Pro Phe Tyr Ser Gln Cys Val Pro
30 35 40

aat gaa aac ctc acc tcc act aac aaa tct tct cac aaa acc acc act 240

Asn Glu Asn Leu Thr Ser Thr Asn Lys Ser Ser His Lys Thr Thr Thr

45 50 55

act gag agt gcc aag aag act acc act act aaa ggt tcc aag aag acc 288

Thr Glu Ser Ala Lys Lys Thr Thr Thr Thr Lys Gly Ser Lys Lys Thr

60 65 70

acc act act gaa gcc tct aag aag acc acc act act gaa gct tcc aag 336

Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Glu Ala Ser Lys

75 80 85

aag acc acc act act gaa gcc tct aag aag acc acc act act act aag 384

Lys Thr Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Thr Lys

90 95 100 105

aag gct tct acc tcc act tcc tct tcc tct tct tct gct tct aca aac 432

Lys Ala Ser Thr Ser Thr Ser Ser Ser Ser Ser Ser Ala Ser Thr Asn

110 115 120

tac tcc gct gtc tct ggt ggt gcc tcc ggt aat ggt gaa acc act cgc 480

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly Asn Gly Glu Thr Thr Arg

125 130 135

tac tgg gat tgt tgt aag cct tct tgc agt tgg ccc ggt aag gct gat 528

Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ser Trp Pro Gly Lys Ala Asp

140 145 150

gtc acc tcc cct gtt ggc tcc tgt aac aag gat ggt aag act ctt gct 576

Val Thr Ser Pro Val Gly Ser Cys Asn Lys Asp Gly Lys Thr Leu Ala

155 160 165

gat aac aac act caa aac ggc tgt gtt ggt ggt agc agc tac acc tgt 624
Asp Asn Asn Thr Gln Asn Gly Cys Val Gly Gly Ser Ser Tyr Thr Cys
170 175 180 185

aat gac aat caa cct tgg gtt gtt agc gac gac ctt gcc tac ggt ttc 672
Asn Asp Asn Gln Pro Trp Val Val Ser Asp Asp Leu Ala Tyr Gly Phe
190 195 200

gcc gct gct tcc att tct ggt ggt agc gaa gct act tgg tgt tgt gcc 720
Ala Ala Ala Ser Ile Ser Gly Gly Ser Glu Ala Thr Trp Cys Cys Ala
205 210 215

tgt ttc gaa ctc aca ttc acc tct act gcc gtc aag ggt aag aag atg 768
Cys Phe Glu Leu Thr Phe Thr Ser Thr Ala Val Lys Gly Lys Lys Met
220 225 230

gtt gtt caa gta acc aac act ggt tct gac ctt ggc tct aac act ggt 816
Val Val Gln Val Thr Asn Thr Gly Ser Asp Leu Gly Ser Asn Thr Gly
235 240 245

gct cac ttt gac ttg caa atg ccc ggt ggt ggt gtt ggt atc tac aat 864
Ala His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Tyr Asn
250 255 260 265

ggt tgt gcc act caa tgg ggt gct ccc acc gat ggt tgg ggt gca aga 912
Gly Cys Ala Thr Gln Trp Gly Ala Pro Thr Asp Gly Trp Gly Ala Arg
270 275 280

tac ggc ggt gtt tct tct gcc tct gac tgt tct aac ctt cct tct gcc 960
Tyr Gly Gly Val Ser Ser Ala Ser Asp Cys Ser Asn Leu Pro Ser Ala
285 290 295

ctt caa gct ggt tgt aag tgg aga ttc ggc tgg ttc aaa aac gct gat 1008
Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn Ala Asp
300 305 310

aac cca acc atg acc tac aaa caa gtt acc tgt ccc aag gct atc act 1056
Asn Pro Thr Met Thr Tyr Lys Gln Val Thr Cys Pro Lys Ala Ile Thr
315 320 325

gcc aag tct ggc tgt tca aga aaa taa 1083
Ala Lys Ser Gly Cys Ser Arg Lys
330 335

<210> 7
<211> 338
<212> PRT
<213> Mucor circinelloides CP99001

<220>
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<222> (-22)...(-1)
<221> mat_peptide
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<400> 7

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-20 -15 -10

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-5 1 5 10

Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr

15 20 25

Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro Gly

30 35 40

Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr Ser

45 50 55

Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr Thr

60 65 70

Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser Thr

75 80 85 90

Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys Val

95 100 105

Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp Asp

110 115 120

Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr Gly

125 130 135

Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala Asn
140 145 150

Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn Asn
155 160 165 170

Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Ala
175 180 185

Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr Glu
190 195 200

Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val Gln
205 210 215

Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu Gln
220 225 230

Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln Trp
235 240 245 250

Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser Ser
255 260 265

Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys
270 275 280

Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr Phe

285 290 295

Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys Glu
300 305 310

Arg Lys
315

<210> 8
<211> 1017
<212> DNA
<213> Mucor circinelloides CP99001

<220>
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<221> mat_peptide
<222> (67)..(1017)

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-20 -15 -10

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Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys
-5 1 5 10

ggt ggc att gga tgg agt gga cct acc tgt tgt gaa agt ggc tct act 144

Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr
15 20 25

tgc gtt gct caa gaa ggc aac aaa tac tac tct caa tgt ctt ccc gga 192
Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro Gly
30 35 40

tcc cac agt aac aat gct ggt aac gct agc agc acc aag aag aca tct 240
Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr Ser
45 50 55

acc aag aca tct act acc acc gcc aag gct act gct act gtc acc acc 288
Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr Thr
60 65 70

aag aca gta acc aag aca act acc aag aca act acc aag act agc act 336
Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser Thr
75 80 85 90

act gcc gct gct tct act tcc acc tct tct tct gct ggt tac aag gtc 384
Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys Val
95 100 105

atc tct ggc ggt aaa tct ggc agt ggt tcc aca act cgt tat tgg gat 432
Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp Asp
110 115 120

tgt tgt aaa gct tct tgc agc tgg cct gga aaa gct tct gtc act ggt 480
Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr Gly

125 130 135

cct gtt gac acc tgt gcc tcc aat ggt atc tct tta tta gat gcc aat 528
Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala Asn
140 145 150

gct caa agt ggt tgt aac ggt ggt aat ggt ttc atg tgt aac aac aac 576
Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn Asn
155 160 165 170

caa cct tgg gct gtc aat gat gag ctc gct tac ggt ttc gct gct gcc 624
Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Ala
175 180 185

tct att gct ggc tcc aac gaa gct gga tgg tgt tgt ggc tgt tat gaa 672
Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr Glu
190 195 200

ttg acc ttc act tct ggc gct gct tct gga aag aag atg gtt gtt caa 720
Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val Gln
205 210 215

gtt acc aac acc ggt ggc gat tta ggc tct aac cac ttt gat ttg caa 768
Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu Gln
220 225 230

atg ccc ggt ggt ggc gtt ggt atc ttc aat ggc tgt gct gct caa tgg 816
Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln Trp
235 240 245 250

ggc gct ccc aat gat ggc tgg gga gct aga tat ggt ggt gtc agc tct 864
Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser Ser
255 260 265

gtc tct gac tgt gcc tct ctt ccc tct gct ctt caa gct ggt tgt aaa 912
Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys
270 275 280

tgg aga ttc aac tgg ttc aag aac tct gat aac cct acc atg acc ttc 960
Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr Phe
285 290 295

aag gaa gtt acc tgt cct gct gaa tta act act cgc tca ggt tgc gaa 1008
Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys Glu
300 305 310

aga aag taa 1017
Arg Lys
315

<210> 9
<211> 387
<212> PRT
<213> Mucor circinelloides CP99001

<220>
<221> sig_peptide
<222> (-22)...(-1)

<221> mat_peptide

<222> (1)...(365)

<400> 9

Met Lys Phe Thr Val Ala Ile Thr Ser Ile Ala Val Ala Leu Ala Leu
-20 -15 -10

Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys
-5 1 5 10

Gly Gly Ile Gly Trp Thr Gly Pro Thr Cys Cys Asp Ala Gly Ser Thr
15 20 25

Cys Lys Ala Gln Lys Asp Asn Lys Tyr Tyr Ser Gln Cys Ile Pro Lys
30 35 40

Pro Lys Gly Ser Ser Ser Ser Ser Ser Cys Ser Ser Val Tyr Ser Gln
45 50 55

Cys Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser
60 65 70

Thr Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro
75 80 85 90

Gly Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr
95 100 105

Ser Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr

110 115 120

Thr Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser
125 130 135

Thr Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys
140 145 150

Val Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp
155 160 165 170

Asp Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr
175 180 185

Gly Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala
190 195 200

Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn
205 210 215

Asn Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala
220 225 230

Ala Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr
235 240 245 250

Glu Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val
255 260 265

Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu
270 275 280

Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln
285 290 295

Trp Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser
300 305 310

Ser Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys
315 320 325 330

Lys Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr
335 340 345

Phe Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys
350 355 360

Glu Arg Lys
365

<210> 10
<211> 1164
<212> DNA
<213> Mucor circinelloides CP99001

<220>
<221> sig_peptide
<222> (1)..(66)

<221> mat_peptide

<222> (67)..(1164)

<400> 10

atg aag ttc acc gtt gct att act tca atc gct gtt gca ctc gct ctc 48
Met Lys Phe Thr Val Ala Ile Thr Ser Ile Ala Val Ala Leu Ala Leu
-20 -15 -10

agc tct tct gct gaa gct gct tct tgc agc tct gtc tat ggt caa tgt 96
Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys
-5 1 5 10

ggt ggc att ggc tgg act ggt cct aca tgt tgt gat gct gga tcg acc 144
Gly Gly Ile Gly Trp Thr Gly Pro Thr Cys Cys Asp Ala Gly Ser Thr
15 20 25

tgt aaa gct caa aag gat aac aaa tat tat tct caa tgt att ccc aaa 192
Cys Lys Ala Gln Lys Asp Asn Lys Tyr Tyr Ser Gln Cys Ile Pro Lys
30 35 40

ccc aag ggt tcc tcc tca tca tca tca tgt agt tcc gtc tat agt caa 240
Pro Lys Gly Ser Ser Ser Ser Ser Ser Cys Ser Ser Val Tyr Ser Gln
45 50 55

tgc ggt ggc att gga tgg agt gga cct acc tgt tgt gaa agt ggc tct 288
Cys Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser
60 65 70

act tgc gtt gct caa gaa ggc aac aaa tac tac tct caa tgt ctt ccc 336

Thr Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro
75 80 85 90

gga tcc cac agt aac aat gct ggt aac gct agc agc acc aag aag aca 384
Gly Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr
95 100 105

tct acc aag aca tct act acc acc gcc aag gct act gct act gtc acc 432
Ser Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr
110 115 120

acc aag aca gta acc aag aca act acc aag aca act acc aag act agc 480
Thr Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser
125 130 135

act act gcc gct gct tct act tcc acc tct tct tct gct ggt tac aag 528
Thr Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys
140 145 150

gtc atc tct ggc ggt aaa tct ggc agt ggt tcc aca act cgt tat tgg 576
Val Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp
155 160 165 170

gat tgt tgt aaa gct tct tgc agc tgg cct gga aaa gct tct gtc act 624
Asp Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr
175 180 185

ggt cct gtt gac acc tgt gcc tcc aat ggt atc tct tta tta gat gcc 672
Gly Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala

190 195 200

aat gct caa agt ggt tgt aac ggt ggt aat ggt ttc atg tgt aac aac 720
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn
205 210 215

aac caa cct tgg gct gtc aat gat gag ctc gct tac ggt ttc gct gct 768
Asn Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala
220 225 230

gcc tct att gct ggc tcc aac gaa gct gga tgg tgt tgt ggc tgt tat 816
Ala Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr
235 240 245 250

gaa ttg acc ttc act tct ggc gct gct tct gga aag aag atg gtt gtt 864
Glu Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val
255 260 265

caa gtt acc aac acc ggt ggc gat tta ggc tct aac cac ttt gat ttg 912
Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu
270 275 280

caa atg ccc ggt ggt ggc gtt ggt atc ttc aat ggc tgt gct gct caa 960
Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln
285 290 295

tgg ggc gct ccc aat gat ggc tgg gga gct aga tat ggt ggt gtc agc 1008
Trp Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser
300 305 310

tct gtc tct gac tgt gcc tct ctt ccc tct gct ctt caa gct ggt tgt 1056
Ser Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys
315 320 325 330

aaa tgg aga ttc aac tgg ttc aag aac tct gat aac cct acc atg acc 1104
Lys Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr
335 340 345

ttc aag gaa gtt acc tgt cct gct gaa tta act act cgc tca ggt tgc 1152
Phe Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys
350 355 360

gaa aga aag taa 1164
Glu Arg Lys
365

<210> 11
<211> 346
<212> PRT
<213> Phycomyces nitens CP99002

<220>
<221> sig_peptide
<222> (-19)...(-1)
<221> mat_peptide
<222> (1)...(327)

<400> 11

Met Lys Phe Ser Ile Ile Ala Ser Ala Leu Leu Leu Ala Ala Ser Ser
-15 -10 -5

Thr Tyr Ala Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys
1 5 10

Met Trp Thr Gly Pro Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly
15 20 25

Ala Glu Asn Asn Glu Trp Tyr Ser Gln Cys Ile Pro Asn Asp Gln Val
30 35 40 45

Gln Gly Asn Pro Lys Thr Thr Thr Thr Thr Thr Thr Lys Ala Ala Thr
50 55 60

Thr Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr
65 70 75

Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr Thr
80 85 90

Lys Thr Thr Thr Lys Thr Thr Thr Thr Lys Ala Ala Thr Thr Thr Ser
95 100 105

Ser Ser Asn Thr Gly Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly Asn
110 115 120 125

Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp
130 135 140

Asp Gly Lys Ala Ser Val Thr Lys Pro Val Leu Thr Cys Ala Lys Asp
145 150 155

Gly Val Ser Arg Leu Gly Ser Asp Val Gln Ser Gly Cys Val Gly Gly
160 165 170

Gln Ala Tyr Met Cys Asn Asp Asn Gln Pro Trp Val Val Asn Asp Asp
175 180 185

Leu Ala Tyr Gly Phe Ala Ala Ala Ser Leu Gly Ser Ala Gly Ala Ser
190 195 200 205

Ala Phe Cys Cys Gly Cys Tyr Glu Leu Thr Phe Thr Asn Thr Ala Val
210 215 220

Ala Gly Lys Lys Phe Val Val Gln Val Thr Asn Thr Gly Asp Asp Leu
225 230 235

Ser Thr Asn His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Tyr
240 245 250

Phe Asn Gly Cys Gln Ser Gln Trp Asn Thr Asn Thr Asp Gly Trp Gly
255 260 265

Ala Arg Tyr Gly Gly Ile Ser Ser Ile Ser Glu Cys Asp Lys Leu Pro
270 275 280 285

Thr Gln Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn

290 295 300

Ala Asp Asn Pro Glu Val Thr Phe Lys Ala Val Thr Cys Pro Ala Glu
305 310 315

Ile Ile Ala Lys Thr Gly Cys Glu Arg Lys
320 325

<210> 12

<211> 1041

<212> DNA

<213> Phycomyces nitens CP99002

<220>

<221> sig_peptide

<222> (1)..(57)

<221> mat_peptide

<222> (58)..(1041)

<400> 12

atg aag ttc tcc atc atc gct tcc gcc ctt ctc ctc gct gcc agc tcc 48
Met Lys Phe Ser Ile Ile Ala Ser Ala Leu Leu Leu Ala Ala Ser Ser
-15 -10 -5

act tac gct gct gaa tgc agc caa ggc tat ggc cag tgt ggt ggc aag 96
Thr Tyr Ala Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys
1 5 10

atg tgg act ggt ccc acc tgc tgc acc tcc ggc ttc acc tgt gta ggt 144

Met Trp Thr Gly Pro Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly
15 20 25

gcc gaa aac aac gag tgg tac tct cag tgt atc ccc aac gat caa gtc 192
Ala Glu Asn Asn Glu Trp Tyr Ser Gln Cys Ile Pro Asn Asp Gln Val
30 35 40 45

cag ggt aac ccc aag acc acc acc acc acc acc acc aag gct gcc act 240
Gln Gly Asn Pro Lys Thr Thr Thr Thr Thr Thr Thr Lys Ala Ala Thr
50 55 60

acc acc aag gct cct gtc acc acc acc aag gcc acc acc acc acc acc 288
Thr Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr
65 70 75

acc aag gcc cct gtc acc acc acc aag gcc act act act acc acc acc 336
Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr Thr
80 85 90

aag acc acc acc aag acc acc acc acc aag gct gcc acc acc acc tcc 384
Lys Thr Thr Thr Lys Thr Thr Thr Thr Lys Ala Ala Thr Thr Thr Ser
95 100 105

tct tcc aac act ggc tac agc ccc att tct ggt ggc ttc tct gga aac 432
Ser Ser Asn Thr Gly Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly Asn
110 115 120 125

ggt cgc act acc cgc tac tgg gat tgc tgc aag ccc tct tgc gcc tgg 480
Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp

130 135 140

gac gga aag gct tct gta act aag cct gta ctc acc tgt gcc aag gat 528
Asp Gly Lys Ala Ser Val Thr Lys Pro Val Leu Thr Cys Ala Lys Asp
145 150 155

ggt gtc agc cgt ctc ggt tcc gat gtc cag agc ggt tgc gtc ggc ggc 576
Gly Val Ser Arg Leu Gly Ser Asp Val Gln Ser Gly Cys Val Gly Gly
160 165 170

cag gcc tac atg tgc aat gac aac cag ccc tgg gtt gtc aat gac gac 624
Gln Ala Tyr Met Cys Asn Asp Asn Gln Pro Trp Val Val Asn Asp Asp
175 180 185

ctt gcc tac ggt ttc gct gct gcc agt ctc ggt agc gcc ggt gcc tct 672
Leu Ala Tyr Gly Phe Ala Ala Ala Ser Leu Gly Ser Ala Gly Ala Ser
190 195 200 205

gca ttc tgc tgc ggc tgt tac gag ctt acc ttc acc aac act gct gtc 720
Ala Phe Cys Cys Gly Cys Tyr Glu Leu Thr Phe Thr Asn Thr Ala Val
210 215 220

gct ggc aag aag ttt gtc gtc cag gtc acc aac acc ggt gat gat ctc 768
Ala Gly Lys Lys Phe Val Val Gln Val Thr Asn Thr Gly Asp Asp Leu
225 230 235

agc acc aac cac ttt gat ttg cag atg ccc ggc ggt ggt gtc ggc tac 816
Ser Thr Asn His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Tyr
240 245 250

ttc aac ggc tgc cag tcc cag tgg aac acc aac acc gat ggc tgg ggt 864
Phe Asn Gly Cys Gln Ser Gln Trp Asn Thr Asn Thr Asp Gly Trp Gly
255 260 265

gct cgc tat ggc ggt att agc tct att tca gag tgc gac aag ctt cct 912
Ala Arg Tyr Gly Gly Ile Ser Ser Ile Ser Glu Cys Asp Lys Leu Pro
270 275 280 285

acc cag ttg cag gct ggt tgc aag tgg aga ttc gga tgg ttc aag aac 960
Thr Gln Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn
290 295 300

gct gac aac cca gag gtc acc ttc aag gct gtt act tgc cct gcc gag 1008
Ala Asp Asn Pro Glu Val Thr Phe Lys Ala Val Thr Cys Pro Ala Glu
305 310 315

atc att gcc aag act ggt tgc gag cgc aag taa 1041
Ile Ile Ala Lys Thr Gly Cys Glu Arg Lys
320 325

<210> 13
<211> 1043
<212> DNA
<213> Artificial Sequence

<220>
<221> sig_peptide
<222> (16)..(84)

<221> mat_peptide

<222> (84)..(1043)

<400> 13

ggatcctggg acaag atg aag ttc atc act atc gcc tcc tcc gcc ctc ctt 51
Met Lys Phe Ile Thr Ile Ala Ser Ser Ala Leu Leu
-20 -15

gcc ctc gcc ctt ggc act gag atg gcc tcc gcc gct gag tgc tcc aag 99
Ala Leu Ala Leu Gly Thr Glu Met Ala Ser Ala Ala Glu Cys Ser Lys
-10 -5 1 5

ctc tac gga cag tgc ggc gga aag aac tgg aac ggc ccc acc tgc tgc 147
Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys
10 15 20

gag agc ggc tcg acc tgc aag gtc tcg aat gac tac tac agc cag tgc 195
Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys
25 30 35

ctg ccg agc ggc tcc tcg gga aac aag tcg agc gag tcg gcc cac aag 243
Leu Pro Ser Gly Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys
40 45 50

aag acc acg acc gct gcc cac aag aag acc acg acc gcc gct cac aag 291
Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys
55 60 65

aag act acg acc gct ccc gcc aag aag acc acg acc gtc gcc aag gct 339

Lys Thr Thr Thr Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala
70 75 80 85

tcg act ccg tcc aac tcg agc agc tcg tct tcg gga aag tac agc gct 387
Ser Thr Pro Ser Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala
90 95 100

gtc agc ggt ggc gct agc ggc aac ggc gtc act acc cgc tac tgg gac 435
Val Ser Gly Gly Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp
105 110 115

tgc tgc aag gct tcg tgc tcg tgg ccc ggc aag gct aac gtc agc tcg 483
Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser
120 125 130

cct gtc aag tcc tgc aac aag gac ggc gtc acc gct ctt agc gac tcc 531
Pro Val Lys Ser Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser
135 140 145

aac gcc cag tcc ggc tgc aac ggc ggc aac tcc tac atg tgc aac gac 579
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp
150 155 160 165

aac cag cca tgg gct gtc aac gac aac ctt gct tac ggt ttc gct gcc 627
Asn Gln Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala
170 175 180

gct gcc att agc ggc ggt ggc gag agc cgc tgg tgc tgc tcc tgc ttc 675
Ala Ala Ile Ser Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe

185 190 195

gag ctc acc ttc acc tcc acc agc gtt gct ggc aag aag atg gtc gtc 723
Glu Leu Thr Phe Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val
200 205 210

cag gtc acc aac act ggc ggt gac ctt ggc agc tcg acc ggt gcc cac 771
Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His
215 220 225

ttc gat ctc cag atg ccc ggc ggc ggc gtc ggc atc ttc aac gga tgc 819
Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys
230 235 240 245

tcg tcc cag tgg ggc gct ccc aac gac ggc tgg ggc tcg cgc tac ggc 867
Ser Ser Gln Trp Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly
250 255 260

ggc atc agc tcc gcc agc gac tgc tcg tcc ctc ccc agc gcc ctc cag 915
Gly Ile Ser Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln
265 270 275

gcc ggc tgc aag tgg cgc ttc aac tgg ttc aag aac gcc gac aac ccg 963
Ala Gly Cys Lys Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro
280 285 290

tcc atg acc tac aag gag gtc acc tgc ccc aag gag atc acc gct aag 1011
Ser Met Thr Tyr Lys Glu Val Thr Cys Pro Lys Glu Ile Thr Ala Lys
295 300 305

acc gga tgc tcg cgc aag taaacgcagg atcc 1043

Thr Gly Cys Ser Arg Lys

310 315

<210> 14

<211> 40

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 14

Ala Glu Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn

1 5 10 15

Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp

20 25 30

Tyr Tyr Ser Gln Cys Leu Pro Ser

35 40

<210> 15

<211> 22

<212> PRT

<213> Mucor circinelloides CP99001

<400> 15

Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys Gly Gly Ile Gly Trp Ser

1 5 10 15

Gly Pro Thr Cys Cys Glu
20

<210> 16
<211> 23
<212> PRT
<213> Phycomyces nitens CP99002

<400> 16
Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys Met Trp Thr
1 5 10 15

Gly Pro Thr Cys Cys Thr Ser
20

<210> 17
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus sequence

<400> 17

Xaa Xaa Xaa Xaa Xaa Xaa Gln Cys Gly Gly Xaa Xaa Xaa Xaa Gly Xaa
1 5 10 15

Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn
20 25 30

Xaa Xaa Tyr Xaa Gln Cys Xaa
35

<210> 18
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus sequence (CBD)

<400> 18
Xaa Xaa Xaa Xaa Xaa Xaa Gln Cys Gly Gly Xaa Xaa Xaa Xaa Gly Xaa
1 5 10 15

Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn
20 25 30

Xaa Xaa Tyr Xaa Gln Cys Xaa
35

<210> 19

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus sequence (CBD)

<400> 19

Cys Ser Xaa Xaa Tyr Xaa Gln Cys Gly Gly Xaa Xaa Trp Xaa Gly Pro
1 5 10 15

Thr Cys Cys Xaa Xaa Gly Xaa Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa
20 25 30

Xaa Tyr Ser Gln Cys Xaa
35

<210> 20

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus sequence (CBD)

<400> 20

Cys Ser Xaa Xaa Tyr Xaa Gln Cys Gly Gly Xaa Xaa Trp Xaa Gly Pro
1 5 10 15

Thr Cys Cys Xaa Xaa Gly Xaa Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa
20 25 30

Xaa Tyr Ser Gln Cys Xaa
35

<210> 21

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus sequence (CBD)

<400> 21

Cys Ser Lys Xaa Tyr Xaa Gln Cys Gly Gly Lys Xaa Trp Xaa Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa
20 25 30

Xaa Tyr Ser Gln Cys Xaa

35

<210> 22

<211> 36

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 22

Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr
20 25 30

Ser Gln Cys Leu
35

<210> 23

<211> 36

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 23

Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asp Trp Asn Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr

20 25 30

Ser Gln Cys Leu
35

<210> 24
<211> 38
<212> PRT
<213> Rhizopus oryzae CP96001

<400> 24
Cys Ser Lys Ala Tyr Tyr Gln Cys Gly Gly Lys Asn Trp Asp Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Val Asp Tyr Pro Asp Asn Pro
20 25 30

Phe Tyr Ser Gln Cys Val
35

<210> 25
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus

sequence (CBD)

<400> 25

Cys Ser Ser Val Tyr Xaa Gln Cys Gly Gly Ile Gly Trp Xaa Gly Pro
1 5 10 15

Thr Cys Cys Xaa Xaa Gly Ser Thr Cys Xaa Ala Gln Xaa Xaa Asn Lys
20 25 30

Tyr Tyr Ser Gln Cys Xaa
35

<210> 26

<211> 38

<212> PRT

<213> Mucor circinelloides CP99001

<400> 26

Cys Ser Ser Val Tyr Gly Gln Cys Gly Gly Ile Gly Trp Ser Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Val Ala Gln Glu Gly Asn Lys
20 25 30

Tyr Tyr Ser Gln Cys Leu
35

<210> 27

<211> 38

<212> PRT

<213> Mucor circinelloides CP99001

<400> 27

Cys Ser Ser Val Tyr Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro
1 5 10 15

Thr Cys Cys Asp Ala Gly Ser Thr Cys Lys Ala Gln Lys Asp Asn Lys
20 25 30

Tyr Tyr Ser Gln Cys Ile
35

<210> 28

<211> 38

<212> PRT

<213> Phycomyces nitens CP99002

<400> 28

Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys Met Trp Thr Gly Pro
1 5 10 15

Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly Ala Glu Asn Asn Glu
20 25 30

Trp Tyr Ser Gln Cys Ile

<210> 29

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus sequence (linker)

<400> 29

Xaa Thr Arg Tyr Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10

<210> 30

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus sequence (linker)

<400> 30

Tyr Xaa Xaa Xaa Ser Gly Gly Xaa Ser Gly

1 5 10

<210> 31

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus sequence (linker)

<400> 31

Tyr Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Gly

1 5 10

<210> 32

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus sequence (linker)

<400> 32

Tyr Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Gly

1 5 10

<210> 33

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 33

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly

1 5 10

<210> 34

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 34

Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly

1 5 10

<210> 35

<211> 10

<212> PRT

<213> Mucor circinelloides CP99001

<400> 35

Tyr Lys Val Ile Ser Gly Gly Lys Ser Gly

1 5 10

<210> 36

<211> 10

<212> PRT

<213> Phycomyces nitens CP99002

<400> 36

Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly

1 5 10

<210> 37

<211> 26

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 37

Ala Lys Ala Ser Thr Pro Ser Asn Ser Ser Ser Ser Ser Ser Gly Lys

1 5 10 15

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly

20 25

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Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys
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Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly
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Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys
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Lys

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Leu Gln

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ggaaagaact gg 132

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<211> 150

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aaggcttcga ctccgtccaa ctcgagcagc tcgtcctc 158

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<210> 96

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